

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 101507,343

Source: PCT

Date Processed by STIC: 4-28-05

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/507,343

DATE: 04/28/2005
TIME: 16:23:13

Input Set : E:\405uspc.app.txt
Output Set: N:\CRF4\04272005\J507343.raw

3 <110> APPLICANT: Ema, Hideo
 4 Nakauchi, Hiromitsu
 5 Osawa, Mitsujiro
 7 <120> TITLE OF INVENTION: PROTEIN SUSTAINING UNDIFFERENTIATED STEM CELLS
 9 <130> FILE REFERENCE: 790086.405USPC
 11 <140> CURRENT APPLICATION NUMBER: US 10/507,343
 C--> 12 <141> CURRENT FILING DATE: 2004-09-10 (PG, 6)
 14 <150> PRIOR APPLICATION NUMBER: PCT/JP02/02265
 15 <151> PRIOR FILING DATE: 2002-03-11
 17 <160> NUMBER OF SEQ ID NOS: 27
 19 <170> SOFTWARE: PatentIn Ver. 2.1
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 1140
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Mus musculus
 26 <400> SEQUENCE: 1
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 28 ctgctccgc tgcgagcgga tgcaggcggc ccacctgagg agagcttgta cctgtggatc 120
 29 gacgccccatc aggcttaggt gtcataagga tttgaagaag acattctgtat tgtctcgag 180
 30 gggaaaatgg cccctttac acatgatttca agggaaagccc aacaaagaat gccagccatt 240
 31 cctgtcaata tccactccat gaattttacc tggcaagctg cggggcaggc agaatacttc 300
 32 tacgagttcc tgtctctgat cttccctggat aaaggcatca tggcagatcc aactgtcaat 360
 33 gtcccttgc tggaaacagt gcctcacaag gcatcagttg ttcaagttgg tttccctgtgt 420
 34 ctcggcaaac aagacggggt agcagcattt gaagtgaatg tgattgtcat gaattctgaa 480
 35 ggcaacacca tccttaggac ccctcagaat gccatcttct taaaacatg tcaacaagct 540
 36 gagtgtcccg gagggtgtcg aaatggaggg tttttaacg aaaggcgggt ctgcgagtgt 600
 37 ccggatgggt tctacgggcc tcaactgttagg aaagccctgt gcataccccg atgtatgaac 660
 38 gtttgtctgt gtgtcactcc tggcttctgc atctgccccctt cggattcta cgggtcaac 720
 39 tgtgacaaag caaactgtctt aaccacactgc tttaatggag ggacctgtctt ttacccggga 780
 40 aaatgtatcc gcccctctgg actcgaggga gagcagtgtg aactcagcaa atgcccccaa 840
 41 ccctggccaa atggaggtaa atgcattgtt aaaagcaagt gtaagtgcggc gaaaggttac 900
 42 caaggagacc tgtgctctaa gcccgtctgc gagcctggct gtggtgccca cggAACCTGC 960
 43 cacgaaccca acaagtgcctt gtgtcgagag ggctggcacg gcagacactg caataagagg 1020
 44 tatggagccca gcctcatgca tgccccggagg ccagcaggcg ccgggctgga ggcacacacg 1080
 45 ctttcactta aaaaggctga ggatagaagg gatccacactg aatccaattt catctggta 1140
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 49 <211> LENGTH: 379
 50 <212> TYPE: PRT
 51 <213> ORGANISM: Mus musculus
 53 <400> SEQUENCE: 2
 54 Met Ala Arg Arg Arg Ala Phe Pro Ala Phe Ala Leu Arg Leu Trp Ser
 55 1 5 10 15
 57 Ile Leu Pro Cys Leu Leu Leu Arg Ala Asp Ala Gly Gln Pro Pro

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61	35	40	45	
63	Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala			
64	50	55	60	
66	Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile			
67	65	70	75	80
69	Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln			
70	85	90	95	
72	Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly			
73	100	105	110	
75	Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro			
76	115	120	125	
78	His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln			
79	130	135	140	
81	Asp Gly Val Ala Ala Phe Glu Val Asn Val Ile Val Met Asn Ser Glu			
82	145	150	155	160
84	Gly Asn Thr Ile Leu Arg Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr			
85	165	170	175	
87	Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys			
88	180	185	190	
90	Asn Glu Arg Arg Val Cys Glu Cys Pro Asp Gly Phe Tyr Gly Pro His			
91	195	200	205	
93	Cys Glu Lys Ala Leu Cys Ile Pro Arg Cys Met Asn Gly Gly Leu Cys			
94	210	215	220	
96	Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn			
97	225	230	235	240
99	Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys			
100	245	250	255	
102	Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln			
103	260	265	270	
105	Cys Glu Leu Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys			
106	275	280	285	
108	Ile Gly Lys Ser Lys Cys Lys Cys Pro Lys Gly Tyr Gln Gly Asp Leu			
109	290	295	300	
111	Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys			
112	305	310	315	320
114	His Glu Pro Asn Lys Cys Gln Cys Arg Glu Gly Trp His Gly Arg His			
115	325	330	335	
117	Cys Asn Lys Arg Tyr Gly Ala Ser Leu Met His Ala Pro Arg Pro Ala			
118	340	345	350	
120	Gly Ala Gly Leu Glu Arg His Thr Pro Ser Leu Lys Lys Ala Glu Asp			
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123	Arg Arg Asp Pro Pro Glu Ser Asn Tyr Ile Trp			
124	370	375		
127	<210> SEQ_ID NO: 3			
128	<211> LENGTH: 1140			
129	<212> TYPE: DNA			
130	<213> ORGANISM: Homo sapiens			

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132 <400> SEQUENCE: 3
133 atggcccgga ggagcgcctt ccctgcccgc gcgcctgtgc tctggagcat cctcctgtgc 60
134 ctgctggcac tgcggcgga ggcggggccg ccgcaggagg agagcctgta cctatggatc 120
135 gatgctcacc aggcaagagt actcatagaa tttgaagaag atatcctgat tgtttcagag 180
136 gggaaaatgg cacctttac acatgatttc agaaaagcgc aacagagaat gccagctatt 240
137 cctgtcaata tccatccat gaattttacc tggcaagctg cagggcaggc agaataacttc 300
138 tatgaattcc tgtccttgcg ctcccgttat aaaggcatca tggcagatcc aaccgtcaat 360
139 gtcctctgc tggAACAGT gcctcacaag gcacatcgatgg ttcaagttgg tttccatgt 420
140 cttggaaaac agatgggtt ggcagcattt gaatgtggatg tgattgttat gaattctgaa 480
141 ggcaacaccca ttctccaaac acctcaaaat gctatcttct ttaaaacatg tctacaagct 540
142 gagtgcccaag gccccggccg aaatggaggc tttttaatgg aaagacgcattt ctgcgagtgt 600
143 cctgatgggt tccacggacc tcactgttag aaagccctt gtaccccacg atgtatgaaat 660
144 gttggacttt gtgtgactcc tggtttctgc atctgcccac ctggattcta tggagtgaac 720
145 tttgacaaag caaaactgctc aaccacctgc ttaatggag ggacctgttt ctaccctgga 780
146 aaatgttattt gcccctcagg actagagggg gagcagtgtg aaatcagcaa atgcccacaa 840
147 ccctgtcgaa atggaggtaa atgcatttgtt aaaagcaaat gtaagtgttc caaagggttac 900
148 cagggagacc tctgttcaaa gcctgtctgc gagcctggct gtggcaca tggAACCTGC 960
149 catgaaccca acaaataccca atgtcaagaa gtttggcatg gaagacactg caataaaagg 1020
150 tacgaagcca gcctcataca tgccctgagg ccagcaggcg cccagctcag gcagcacacg 1080
151 cttcactta aaaaggccga ggagcggcgg gatccacctg aatccaatta catctggta 1140
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155 <211> LENGTH: 379
156 <212> TYPE: PRT
157 <213> ORGANISM: Homo sapiens
159 <400> SEQUENCE: 4
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163 Ile Leu Leu Cys Leu Leu Ala Leu Arg Ala Glu Ala Gly Pro Pro Gln
164 20 25 30
166 Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu
167 35 40 45
169 Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
170 50 55 60
172 Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile
173 65 70 75 80
175 Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln
176 85 90 95
178 Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly
179 100 105 110
181 Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro
182 115 120 125
184 His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln
185 130 135 140
187 Asp Gly Val Ala Ala Phe Glu Val Asp Val Ile Val Met Asn Ser Glu
188 145 150 155 160
190 Gly Asn Thr Ile Leu Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr
191 165 170 175
193 Cys Leu Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys
194 180 185 190

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196 Asn Glu Arg Arg Ile Cys Glu Cys Pro Asp Gly Phe His Gly Pro His
197 195 200 205
199 Cys Glu Lys Ala Leu Cys Thr Pro Arg Cys Met Asn Gly Gly Leu Cys
200 210 215 220
202 Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn
203 225 230 235 240
205 Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys
206 245 250 255
208 Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln
209 260 265 270
211 Cys Glu Ile Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys
212 275 280 285
214 Ile Gly Lys Ser Lys Cys Lys Cys Ser Lys Gly Tyr Gln Gly Asp Leu
215 290 295 300
217 Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys
218 305 310 315 320
220 His Glu Pro Asn Lys Cys Gln Cys Gln Glu Gly Trp His Gly Arg His
221 325 330 335
223 Cys Asn Lys Arg Tyr Glu Ala Ser Leu Ile His Ala Leu Arg Pro Ala
224 340 345 350
226 Gly Ala Gln Leu Arg Gln His Thr Pro Ser Leu Lys Lys Ala Glu Glu
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230 370 375
233 <210> SEQ ID NO: 5
234 <211> LENGTH: 1098
235 <212> TYPE: DNA
236 <213> ORGANISM: Rattus norvegicus
238 <400> SEQUENCE: 5
239 atggcccgga gaagagcctt ccctgctttc gtgcgtccggc tctggaggcat cctacccgtgc 60
240 ctgctccctgc tacgagcggga tgcaggcgag ccggccagagg agagcttgta cctgtggatc 120
241 gacgcccatac aggccagagt actcatagga tttgaagaag atattctgtat tgtctcggag 180
242 gggaaaatgg ccccccttac acatgatttc agggaaagccc aacaaagaat gccagccatt 240
243 cccgtcaata tccactccat gaattttacc tggcaagctt cagggcaggc agagtacttc 300
244 tatgagttcc tgcgtctgcg ctcgctggat aaaggcatca tggcagaccc aactgtcaat 360
245 gtcctcgcc tggAACAGT gcctcacaaag gcacatggat ttcaagttgg tttccctgtgt 420
246 ctcggcaaac aggatgggtt ggcagcattt gaagtgaatg tgattgtcat gaattctgaa 480
247 ggcaacccca tccttcggac ccctcaaaat gctatcttct ttaaaacatg tcaacaagct 540
248 gagtgcccaag gagggtgtcg aatggaggc tttttaacg aaaggcggtt ctgcgagtgt 600
249 cccgatgggt tctatggacc tcactgttag aaagccctct gcataccctcg atgtatgaac 660
250 ggtggctgt gtgtcaactcc tggcttctgc atctggccgc ctggattcta cggtgtcaac 720
251 tttgtacaaat caaatgttc ggcacactgc tttatggag ggacctgttt ttacccagga 780
252 aatgttattt gccctccagg acttgaggga gagcagtgtg aactcagcaa gtggcccca 840
253 ccctgccgaa acggaggtaa atgcattggt aaaagcaagt ctgtctgcga gcctggctgc 900
254 ggtgcccattt gAACCTGCCA cgaacccaaac aaatgccagt gtcgagaggg ctggcatggg 960
255 agacactgca ataaaaggta cggagccagc ctcatgcattt ccccgaggcc agcaggcgcc 1020
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257 tccaaattaca tctggtga 1098
260 <210> SEQ ID NO: 6

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Input Set : E:\405uspc.app.txt
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261 <211> LENGTH: 365
 262 <212> TYPE: PRT
 263 <213> ORGANISM: Rattus norvegicus
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 270 20 25 30
 272 Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu
 273 35 40 45
 275 Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
 276 50 55 60
 278 Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile
 279 65 70 75 80
 281 Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ser Gly Gln
 282 85 90 95
 284 Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly
 285 100 105 110
 287 Ile Met Ala Asp Pro Thr Val Asn Val Pro Arg Leu Gly Thr Val Pro
 288 115 120 125
 290 His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln
 291 130 135 140
 293 Asp Gly Val Ala Ala Phe Glu Val Asn Val Ile Val Met Asn Ser Glu
 294 145 150 155 160
 296 Gly Asn Pro Ile Leu Arg Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr
 297 165 170 175
 299 Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys
 300 180 185 190
 302 Asn Glu Arg Arg Val Cys Glu Cys Pro Asp Gly Phe Tyr Gly Pro His
 303 195 200 205
 305 Cys Glu Lys Ala Leu Cys Ile Pro Arg Cys Met Asn Gly Gly Leu Cys
 306 210 215 220
 308 Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn
 309 225 230 235 240
 311 Cys Asp Lys Ala Asn Cys Ser Ala Thr Cys Phe Asn Gly Gly Thr Cys
 312 245 250 255
 314 Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln
 315 260 265 270
 317 Cys Glu Leu Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys
 318 275 280 285
 320 Ile Gly Lys Ser Lys Ser Val Cys Glu Pro Gly Cys Gly Ala His Gly
 321 290 295 300
 323 Thr Cys His Glu Pro Asn Lys Cys Gln Cys Arg Glu Gly Trp His Gly
 324 305 310 315 320
 326 Arg His Cys Asn Lys Arg Tyr Gly Ala Ser Leu Met His Ala Pro Arg
 327 325 330 335
 329 Pro Ala Gly Ala Gly Leu Glu Arg His Thr Pro Ser Leu Lys Lys Ala
 330 340 345 350
 332 Glu Gly Arg Arg Asp Pro Pro Glu Ser Asn Tyr Ile Trp

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 04/28/2005
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Input Set : E:\405uspc.app.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:11; N Pos. 12,15,18
Seq#:12; N Pos. 4,7,10,16,22
Seq#:26; Xaa Pos. 2,3,4,6,7,8,9,10,12,13,14,15,16,18,20,21,22,23,24,25,26
Seq#:26; Xaa Pos. 27,29,30,31,32
Seq#:27; Xaa Pos. 2,3,4,5,6,7,8,10,11,12,13,15,16,17,18,19,20,21,22,23,24
Seq#:27; Xaa Pos. 26,28,29,30,31,32,33,34,35

VERIFICATION SUMMARY
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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:563 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:575 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:579 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:580 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
L:1288 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1293 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:1294 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:0
M:341 Repeated in SeqNo=26
L:1309 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1314 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:27
L:1315 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:0
M:341 Repeated in SeqNo=27